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(54) Title: FRAMEWORK MUTATED ANTIBODIES AND THEIR PREPARATION			
(57) Abstract			
<p>An altered antibody chain is produced in which the CDR's of the variable domain of the chain are derived from a first mammalian species. The framework-encoding regions of DNA encoding the variable domain of the first species are mutated so that the mutated framework-encoding regions encode a framework derived from a second different mammalian species. The or each constant domain of the antibody chain, if present, are also derived from the second mammalian species. An antibody which is capable of binding to human CD4 antigen is also provided together with a pharmaceutical composition comprising the antibody.</p>			

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FRAMEWORK MUTATED ANTIBODIES AND THEIR PREPARATION

The present invention relates to altered antibodies and their preparation. The invention is typically applicable to the production of humanised antibodies.

- 5 Antibodies typically comprise two heavy chains linked together by disulphide bonds and two light chains. Each light chain is linked to a respective heavy chain by disulphide bonds. Each heavy chain has at one end a variable domain followed by a number of constant domains.
- 10 Each light chain has a variable domain at one end and a constant domain at its other end. The light chain variable domain is aligned with the variable domain of the heavy chain. The light chain constant domain is aligned with the first constant domain of the heavy chain. The constant domains in the light and heavy chains are not involved directly in binding the antibody to antigen.
- 15

The variable domains of each pair of light and heavy chains form the antigen binding site. The domains on the light and heavy chains have the same general structure and each domain comprises a framework of four regions, whose sequences are relatively conserved, connected by three complementarity determining regions (CDRs). The four framework regions largely adopt a beta-sheet conformation and the CDRs form loops connecting, and in some cases forming part of, the beta-sheet structure. The CDRs are held in close proximity by the framework regions and, with the CDRs from the other domain, contribute to the formation of the antigen binding site.

The preparation of an altered antibody in which the CDRs are derived from a different species than the framework of the antibody's variable domains is disclosed in EP-A-0239400. The CDRs may be derived from a rat or mouse monoclonal antibody. The framework of the variable domains, and the constant domains, of the altered antibody may be derived from a human antibody. Such a humanised

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antibody elicits a negligible immune response when administered to a human compared to the immune response mounted by a human against a rat or mouse antibody. Humanised CAMPATH-1 antibody is disclosed in EP-A-0328404.

5 We have now devised a new way of preparing an altered antibody. In contrast to previous proposals, this involves altering the framework of a variable domain rather than the CDRs. This approach has the advantages that it does not require a pre-existing cDNA encoding, for example, a human
10 framework to which to reshape and that it is technically easier than prior methodologies.

Accordingly, the present invention provides a process for the preparation of an antibody chain in which the CDRs of the variable domain of the antibody chain are derived
15 from a first mammalian species and the framework of the variable domain and, if present, the or each constant domain of the antibody chain are derived from a second different mammalian species, which process comprises:

(i) mutating the framework-encoding regions of DNA
20 encoding a variable domain of an antibody chain of the said first species such that the mutated framework-encoding regions encode the said framework derived from the said second species; and
25 (ii) expressing the said antibody chain utilising the mutated DNA from step (i).

A variable domain of either or both chains of an antibody can therefore be altered by:

(a) determining the nucleotide and predicted amino acid sequence of a variable domain of a selected antibody chain
30 of the said first species;
(b) determining the antibody framework to which the framework of the said variable domain is to be altered;
(c) mutating the framework-encoding regions of DNA encoding the said variable domain such that the mutated

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framework-encoding regions encode the framework determined upon in step (b);

(d) linking the mutated DNA obtained in step (c) to DNA encoding a constant domain of the said second species and

5 cloning the DNA into an expression vector; and

(e) introducing the expression vector into a compatible host cell and culturing the host cell under such conditions that antibody chain is expressed.

The antibody chain may be co-expressed with a

10 complementary antibody chain. At least the framework of the variable domain and the or each constant domain of the complementary chain generally are derived from the said second species also. A light chain and a heavy chain may be co-expressed. Either or both chains may have been

15 prepared by the process of the invention. Preferably the CDRs of both chains are derived from the same selected antibody. An antibody comprising both expressed chains can be recovered.

The antibody preferably has the structure of a natural

20 antibody or a fragment thereof. The antibody may therefore comprise a complete antibody, a $(\text{Fab}')_2$ fragment, a Fab fragment, a light chain dimer or a heavy chain. The antibody may be an IgG such as an IgG1, IgG2, IgG3 or IgG4 IgM, IgA, IgE or IgD. Alternatively, the antibody may be a

25 chimaeric antibody of the type described in WO 86/01533.

A chimaeric antibody according to WO 86/01533 comprises an antigen binding region and a non-immunoglobulin region. The antigen binding region is an antibody light chain variable domain or heavy chain variable domain. Typically,

30 the chimaeric antibody comprises both light and heavy chain variable domains. The non-immunoglobulin region is fused at its C-terminus to the antigen binding region. The non-immunoglobulin region is typically a non-immunoglobulin protein and may be an enzyme region, a region derived from

35 a protein having known binding specificity, from a protein

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toxin or indeed from any protein expressed by a gene. The two regions of the chimaeric antibody may be connected via a cleavable linker sequence.

The invention is preferably employed to humanise an antibody, typically a monoclonal antibody and, for example, a rat or mouse antibody. The framework and constant domains of the resulting antibody are therefore human framework and constant domains whilst the CDRs of the light and/or heavy chain of the antibody are rat or mouse CDRs.

10 Preferably all CDRs are rat or mouse CDRs. The antibody may be a human IgG such as IgG1, IgG2, IgG3, IgG4; IgM; IgA; IgE or IgD carrying rat or mouse CDRs.

The process of the invention is carried out in such a way that the resulting antibody retains the antigen binding capability of the antibody from which it is derived. An antibody is reshaped according to the invention by mutating the framework-encoding regions of DNA coding for the variable domains of the antibody. This antibody and the reshaped antibody should both be capable of binding to the 20 same antigen.

The starting antibody is typically an antibody of a selected specificity. In order to ensure that this specificity is retained, the variable domain framework of the antibody is preferably reshaped to about the closest 25 variable domain framework of an antibody of another species. By "about the closest" is meant about the most homologous in terms of amino acid sequences. Preferably there is a homology of at least 50% between the two variable domains.

30 There are four general steps to reshape a monoclonal antibody. These are:

(1) determining the nucleotide and predicted amino acid sequence of the starting antibody light and heavy chain variable domains;

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(2) designing the reshaped antibody, i.e. deciding which antibody framework region to use during the reshaping process;

5 (3) the actual reshaping methodologies/techniques; and
(4) the transfection and expression of the reshaped antibody.

These four steps are explained below in the context of humanising an antibody. However, they may equally well be applied when reshaping to an antibody of a non-human
10 species.

Step 1: Determining the nucleotide and predicted amino acid sequence of the antibody light and heavy chain variable domains

To reshape an antibody only the amino acid sequence of
15 antibody's heavy and light chain variable domains needs to be known. The sequence of the constant domains is irrelevant because these do not contribute to the reshaping strategy. The simplest method of determining an antibody's variable domain amino acid sequence is from cloned cDNA
20 encoding the heavy and light chain variable domain.

There are two general methods for cloning a given antibody's heavy and light chain variable domain cDNAs: (1) via a conventional cDNA library, or (2) via the polymerase chain reaction (PCR). Both of these methods are widely
25 known. Given the nucleotide sequence of the cDNAs, it is a simple matter to translate this information into the predicted amino acid sequence of the antibody variable domains.

30 Step 2: Designing the reshaped antibody

There are several factors to consider in deciding which human antibody sequence to use during the reshaping. The reshaping of light and heavy chains are considered independently of one another, but the reasoning is
35 basically similar for each.

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This selection process is based on the following rationale: A given antibody's antigen specificity and affinity is primarily determined by the amino acid sequence of the variable region CDRs. Variable domain framework residues have little or no direct contribution. The primary function of the framework regions is to hold the CDRs in their proper spacial orientation to recognize antigen. Thus the substitution of rodent CDRs into a human variable domain framework is most likely to result in retention of their correct spacial orientation if the human variable domain is highly homologous to the rodent variable domain from which they originated. A human variable domain should preferably be chosen therefore that is highly homologous to the rodent variable domain(s).

15 A suitable human antibody variable domain sequence can be selected as follows:

1. Using a computer program, search all available protein (and DNA) databases for those human antibody variable domain sequences that are most homologous to the rodent antibody variable domains. This can be easily accomplished with a program called FASTA but other suitable programs are available. The output of a suitable program is a list of sequences most homologous to the rodent antibody, the percent homology to each sequence, and an alignment of each sequence to the rodent sequence. This is done independently for both the heavy and light chain variable domain sequences. The above analyses are more easily accomplished if customized sub-databases are first created that only include human immunoglobulin sequences. This has two benefits. First, the actual computational time is greatly reduced because analyses are restricted to only those sequences of interest rather than all the sequences in the databases. The second benefit is that, by restricting analyses to only human immunoglobulin

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sequences, the output will not be cluttered by the presence of rodent immunoglobulin sequences. There are far more rodent immunoglobulin sequences in databases than there are human.

- 5 2. List the human antibody variable domain sequences that have the most overall homology to the rodent antibody variable domain (from above). Do not make a distinction between homology within the framework regions and CDRs. Consider the overall homology.
- 10 3. Eliminate from consideration those human sequences that have CDRs that are a different length than those of the rodent CDRs. This rule does not apply to CDR 3, because the length of this CDR is normally quite variable. Also, there are sometimes no or very few human sequences that have the same CDR lengths as that of the rodent antibody. If this is the case, this rule can be loosened, and human sequences with one or more differences in CDR length can be allowed.
- 15 4. From the remaining human variable domains, the one is selected that is most homologous to that of the rodent.
- 20 5. The actual reshaped antibody (the end result) should contain CDRs derived from the rodent antibody and a variable domain framework from the human antibody chosen above.

25 Step 3: The actual reshaping methodologies/techniques
A cDNA encoding the desired reshaped antibody is preferably made beginning with the rodent cDNA from which the rodent antibody variable domain sequence(s) was originally determined. The rodent variable domain amino acid sequence is compared to that of the chosen human antibody variable domain sequence. The residues in the rodent variable domain framework are marked that need to be changed to the corresponding residue in the human to make the rodent framework identical to that of the human

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framework. There may also be residues that need adding to or deleting from the rodent framework sequence to make it identical to that of the human.

Oligonucleotides are synthesised that can be used to 5 mutagenize the rodent variable domain framework to contain the desired residues. Those oligonucleotides can be of any convenient size. One is normally only limited in length by the capabilities of the particular synthesizer one has available. The method of oligonucleotide-directed in vitro 10 mutagenesis is well known.

The advantages of this method of reshaping as opposed to splicing CDRs into a human framework are that (1) this method does not require a pre-existing cDNA encoding the human framework to which to reshape and (2) splicing CDRs 15 is technically more difficult because there is usually a large region of poor homology between the mutagenic oligonucleotide and the human antibody variable domain. This is not so much a problem with the method of splicing human framework residues onto a rodent variable domain because 20 there is no need for a pre-existing cDNA encoding the human variable domain. The method starts instead with the rodent cDNA sequence. Also, splicing framework regions is technically easier because there is a high degree of homology between the mutagenic oligonucleotide and the 25 rodent variable domain framework. This is true because a human antibody variable domain framework has been selected that is most homologous to that of the rodent.

The advantage of the present method of reshaping as opposed to synthesizing the entire reshaped version from 30 scratch is that it is technically easier. Synthesizing a reshaped variable domain from scratch requires several more oligonucleotides, several days more work, and technical difficulties are more likely to arise.

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Step 4: The transfection and expression of the reshaped antibody

Following the mutagenesis reactions to reshape the antibody, the cDNAs are linked to the appropriate DNA encoding light or heavy chain constant region, cloned into an expression vector, and transfected into mammalian cells. These steps can be carried out in routine fashion. A reshaped antibody may therefore be prepared by a process comprising:

- 10 a) preparing a first replicable expression vector including a suitable promoter operably linked to a DNA sequence which encodes at least a variable domain of an Ig heavy or light chain, the variable domain comprising framework regions from a first antibody and CDRs comprising at least parts of the CDRs from a second antibody of different specificity;
- 15 b) if necessary, preparing a second replicable expression vector including a suitable promoter operably linked to a DNA sequence which encodes at least the variable domain of a complementary Ig light or heavy chain respectively;
- 20 c) transforming a cell line with the first or both prepared vectors; and
- 25 d) culturing said transformed cell line to produce said altered antibody.

Preferably the DNA sequence in step a) encodes both the variable domain and the or each constant domain of the antibody chain, the or each constant domain being derived from the first antibody. The antibody can be recovered and purified. The cell line which is transformed to produce the altered antibody may be a Chinese Hamster Ovary (CHO) cell line or an immortalised mammalian cell line, which is advantageously of lymphoid origin, such as a myeloma, hybridoma, trioma or quadroma cell line. The cell line may also comprise a normal lymphoid cell, such as a B-cell,

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which has been immortalised by transformation with a virus, such as the Epstein-Barr virus. Most preferably, the immortalised cell line is a myeloma cell line or a derivative thereof.

5 Although the cell line used to produce the altered antibody is preferably a mammalian cell line, any other suitable cell line, such as a bacterial cell line or a yeast cell line, may alternatively be used. In particular, it is envisaged that E. coli - derived bacterial strains
10 could be used.

It is known that some immortalised lymphoid cell lines, such as myeloma cell lines, in their normal state secrete isolated Ig light or heavy chains. If such a cell line is transformed with the vector prepared in step (a) it will
15 not be necessary to carry out step (b) of the process, provided that the normally secreted chain is complementary to the variable domain of the Ig chain encoded by the vector prepared in step (a).

However, where the immortalised cell line does not
20 secrete or does not secrete a complementary chain, it will be necessary to carry out step (b). This step may be carried out by further manipulating the vector produced in step (a) so that this vector encodes not only the variable domain of an altered antibody light or heavy chain, but
25 also the complementary variable domain.

Alternatively, step (b) is carried out by preparing a second vector which is used to transform the immortalised cell line. This alternative leads to easier construct preparation, but may be less preferred than the first
30 alternative in that it may not lead to as efficient production of antibody.

In the case where the immortalised cell line secretes a complementary light or heavy chain, the transformed cell line may be produced for example by transforming a suitable
35 bacterial cell with the vector and then fusing the

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bacterial cell with the immortalised cell line by spheroplast fusion. Alternatively, the DNA may be directly introduced into the immortalised cell line by electroporation or other suitable method.

5 An antibody is consequently produced in which CDRs of a variable domain of an antibody chain are homologous with the corresponding CDRs of an antibody of a first mammalian species and in which the framework of the variable domain and the constant domains of the antibody are homologous
10 with the corresponding framework and constant domains of an antibody of a second, different, mammalian species. Typically, all three CDRs of the variable domain of a light or heavy chain are derived from the first species.

The present process has been applied to obtain an
15 antibody against human CD4 antigen. Accordingly, the invention also provides an antibody which is capable of binding to human CD4 antigen, in which the CDRs of the light chain of the antibody have the amino acid sequences:

CDR1: LASEDIYSDL
20 CDR2: NTDTLQN
CDR3: QQYNNYPWT,

in which the CDRs of the heavy chain of the antibody have the amino acid sequences:

CDR1: NYGMA
25 CDR2: TISHDGSDTYFRDSVK
CDR3: QGTIAGIRH, and

in which the framework of the variable domain and, if present, the or each constant domain of each chain are derived from a mammalian non-rat species.

30 The antibody preferably has the structure of a natural antibody or a fragment thereof. The antibody may therefore comprise a complete antibody, a $(Fab')_2$ fragment, a Fab fragment, a light chain dimer or a heavy chain.

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The antibody may be an IgG such as IgG1, IgG2, IgG3 or IgG4 IgM, IgA, IgE or IgD. Alternatively, the antibody may be a chimaeric antibody of the type described in WO 86/01533.

5 A chimaeric antibody according to WO 86/01533 comprises an antigen binding region and a non-immunoglobulin region. The antigen binding region is an antibody light chain variable domain or heavy chain variable domain. Typically the chimaeric antibody comprises both light and heavy chain 10 variable domains. The non-immunoglobulin region is fused at its C-terminus to the antigen binding region. The non-immunoglobulin region is typically a non-immunoglobulin protein and may be an enzyme region, a region derived from a protein having known binding specificity, from a protein 15 toxin or indeed from any protein expressed by a gene. The two regions of the chimaeric antibody may be connected via a cleavable linker sequence.

The invention is preferably employed to humanise a CD4 antibody such as a rat or mouse CD4 antibody. The 20 framework and the constant domains of the resulting antibody are therefore human framework and constant domains whilst the CDRs of the light and/or heavy chain of the antibody are rat or mouse CDRs. Preferably all CDRs are rat or mouse CDRs. The antibody may be a human IgG such as 25 IgG1, IgG2, IgG3, IgG4; IgM; IgA; IgE or IgD carrying rat or mouse CDRs.

30 Preferably the framework of the antibody heavy chain is homologous to the corresponding framework of the human antibody KOL (Schmidt *et al*, Hoppe-Seyler's Z. Physiol. Chem., 364 713-747, 1983). The sixth residue of framework 4 in this case is suitably Thr or Pro, preferably Thr. This residue is the 121st residue in the KOL antibody heavy chain variable region (Schmidt *et al*, 1983), and is identified as residue 108 by Kabat (Kabat *et al*, "Sequences 35 of proteins of immunological interest", US Dept of Health

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and Human Services, US Government Printing Office, 1987). Alternatively, the framework of the antibody heavy chain is homologous to the corresponding framework of the human antibody NEW (Saul *et al*, J. Biol. Chem. 253: 585-597, 5 1978). The final residue of framework 1 in this case is suitably Ser or Thr, preferably Ser. This residue is at position 30 (Kabat *et al*, 1987). Preferably the framework of the antibody light chain is homologous to the variable domain framework of the protein REI (Epp *et al*, Eur. J. 10 Biochem., 45, 513-524, 1974).

The framework regions of one or both chains of a CD4 antibody can be reshaped by the present process.

Alternatively, one or both chains of a CD4 antibody may be reshaped by the procedure described in EP-A-0239400. The 15 procedure of EP-A-0239400 involves replacing CDRs rather than the replacement of frameworks. The CDRs are grafted onto a framework derived from a mammalian non-rat species, typically a human. This may be achieved by oligonucleotide-directed *in vitro* mutagenesis of the CDR- 20 encoding regions of an antibody chain, light or heavy, from a mammalian non-rat species. The oligonucleotides in such an instance are selected so that the resulting CDR-grafted antibody has the light chain CDRs 1 to 3 and the heavy chain CDRs 1 to 3 shown above.

25 The reshaped CD4 antibody can be used to induce tolerance to an antigen. It can be used to alleviate autoimmune diseases such as rheumatoid arthritis. It can be used to prevent graft rejection. Tolerance to a graft such as an organ graft or a bone marrow transplantation can 30 be achieved. Also, the reshaped CD4 antibody might be used to alleviate allergies. Tolerance to allergens could be achieved.

The CD4 antibody may be depleting or non-depleting. A depleting antibody is an antibody which depletes more than

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50%, for example from 90 to 99%, of target cells in vivo. A non-depleting antibody depletes fewer than 50%, for example, from 10 to 25% and preferably less than 10% of target cells in vivo. A CD4 antibody may be administered 5 alone or may be co-administered with a non-depleting or depleting CD8 antibody. The CD4 antibody, depleting or non-depleting, and CD8 monoclonal antibody, depleting or non-depleting, may be administered sequentially in any order or may be administered simultaneously. An additional 10 antibody, drug or protein may be administered before, during or after administration of the antibodies.

A CD4 antibody and, indeed, a CD8 antibody as appropriate are given parenterally, for example intravenously. The antibody may be administered by 15 injection or by infusion. For this purpose the antibody is formulated in a pharmaceutical composition further comprising a pharmaceutically acceptable carrier or diluent. Any appropriate carrier or diluent may be employed, for example phosphate-buffered saline solution.

20 The amount of non-depleting or depleting CD4 and, if desired, CD8 antibody administered to a patient depends upon a variety of factors including the age and weight of a patient, the condition which is being treated and the antigen(s) to which it is desired to induce tolerance. In 25 a model mouse system from 1 μ g to 2mg, preferably from 400 μ g to 1mg, of a mAb is administered at any one time. In humans from 3 to 500mg, for example from 5 to 200mg, of antibody may be administered at any one time. Many such doses may be given over a period of several weeks, 30 typically 3 weeks.

A foreign antigen(s) to which it is desired to induce tolerance can be administered to a host before, during, or after a course of CD4 antibody (depleting or non-depleting) and/or CD8 antibody (depleting or non-depleting). 35 Typically, however, the antigen(s) is administered one week

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after commencement of antibody administration, and is terminated three weeks before the last antibody administration.

Tolerance can therefore be induced to an antigen in a host by administering non-depleting or depleting CD4 and CD8 mAbs and, under cover of the mAbs, the antigen. A patient may be operated on surgically under cover of the non-depleting or depleting CD4 and CD8 mAbs to be given a tissue transplant such as an organ graft or a bone marrow transplant. Also, tolerance may be induced to an antigen already possessed by a subject. Long term specific tolerance can be induced to a self antigen or antigens in order to treat autoimmune disease such as multiple sclerosis or rheumatoid arthritis. The condition of a patient suffering from autoimmune disease can therefore be alleviated.

The following Example illustrates the invention. In the accompanying drawings:

Figure 1: shows the nucleotide and predicted amino acid sequence of rat CD4 antibody light chain variable region. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins, respectively. Base pairs 1-269 (HindIII-PvuII) and 577-620 ([BglII/BclI]-BamHI) are part of the vector M13V_KPCR3, while base pairs 270-576 are from the PCR product of the CD4 antibody light chain variable region (V_L). CDRs (boxes) were identified by comparison to known immunological sequences (Kabat *et al*, "Sequences of proteins of immunological interest, US Dept of Health and Human Services, US Government Printing Office, 1987).

Figure 2: shows the nucleotide and predicted amino acid sequence of the reshaped CAMPATH-1 antibody light chain cDNA. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins, respectively. CDRs are identified by boxes.

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Figure 3: shows the nucleotide and predicted amino acid sequence of the reshaped CD4 antibody light chain cDNA CD4V_LREI. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right 5 margins, respectively. CDRs are identified by boxes.

Figure 4: shows the nucleotide and predicted amino acid sequence of rat CD4 antibody heavy chain variable region. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins, 10 respectively. CDRs are identified by boxes. Base pairs 1-272 (HindIII-PstI) and 603-817 (BstEII-BamHI) are part of the vector M13V_HPCR1, while base pairs 273-602 are from the PCR product of the CD4 antibody heavy chain variable region (V_H).

15 Figure 5: shows the nucleotide and predicted amino acid sequence of the reshaped CAMPATH-1 antibody heavy chain cDNA. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins, respectively. CDRs are identified by boxes.

20 Figure 6: shows the nucleotide and predicted amino acid sequence of the reshaped CD4 antibody heavy chain cDNA CD4V_HNEW-Thr³⁰. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins, respectively. CDRs are identified by 25 boxes.

Figure 7: shows the nucleotide and predicted amino acid sequence of the reshaped CD4 antibody heavy chain cDNA CD4V_HNEW-Ser³⁰. The number of the first and last amino acid or nucleotide in each line is indicated in the left 30 and right margins, respectively. CDRs are identified by boxes.

Figure 8: shows the heavy chain variable (V) region amino acid sequence of the human myeloma protein KOL. CDRs are identified by boxes. This sequence is taken from the 35 Swiss-Prot protein sequence database.

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Figure 9: shows the nucleotide and predicted amino acid sequence of the reshaped CD4 antibody heavy chain V region CD4V_HKOL-Pro¹¹³. The number of the first and last amino acid or nucleotide in each line is indicated in the left 5 and right margins, respectively. CDRs are identified by boxes.

Figure 10: shows the nucleotide and predicted amino acid sequence of the reshaped CD4 antibody heavy chain V region CD4V_HKOL-Pro¹¹³ without immunoglobulin promoter. The 10 number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins, respectively. CDRs are identified by boxes.

Figure 11: shows the nucleotide and predicted amino acid sequence of the reshaped CD4 antibody heavy chain V region 15 CD4V_HKOL-Thr¹¹³. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins, respectively. CDRs are identified by boxes.

Figure 12: shows the nucleotide and predicted amino acid 20 sequence of the reshaped CD4 antibody heavy chain V region CD4V_HKOL-Thr¹¹³ without immunoglobulin promoter. The number of the first and last amino acid or nucleotide in each line is indicated in the left and right margins, respectively. CDRs are identified by boxes.

25 Figure 13: shows the results of an ELISA that compares the avidity of YNB46.1.8 and CD4V_HKOL-Thr¹¹³ antibodies. The X-axis indicates the concentration (μ g/ml) of YNB46.1.8 (triangles) or CD4V_HKOL-Thr¹¹³ (circles) antibody. The Y-axis indicates the optical density at 492 nanometers.

EXAMPLE1. MATERIALS AND METHODS

Isolation of monoclonal antibody. The rat-derived anti-human CD4 antibody, clone YNB46.1.8 (IgG_{2b}, kappa light chain serotype), was the result of fusion between a rat splenocyte and the Lou strain rat myeloma cell line Y3-Ag 1.2.3 (Galfre *et al.*, *Nature*, **277**: 131-133, 1979) and was selected by its binding to a rat T cell line NB2-6TG stably transfected with an expression vector containing a complementary DNA (cDNA) encoding the human CD4 antigen (Madden *et al.*, *Cell*, **42**: 93-104, 1985). Antibody was purified by high pressure liquid chromatography (HPLC).

Isolation of Antibody Variable Regions. cDNAs encoding the V_L and V_H regions of the CD4 antibody were isolated by a polymerase chain reaction (PCR)-based method (Orlandi *et al.*, *PNAS USA*, **86**: 3833-3837, 1989) with some modifications. Total RNA was isolated from hybridoma cells by the guanidine thiocyanate method (Chirgwin *et al.*, *Biochemistry*, **18**: 5294, 1979), and poly(A)⁺ RNA was isolated by passage of total RNA through and elution from an oligo(dT)-cellulose column (Aviv and Leder *PNAS USA* **69**: 1408, 1972). Poly(A)⁺ RNA was heated at 70°C for 5 minutes and cooled on ice just prior to use. A 25μl first strand synthesis reaction consisted of 5μg poly(A)⁺ RNA, 250 μM each dNTP, 50 mM Tris.HCl (pH 8.2 at 42°C), 10 mM MgCl₂, 100 mM KCl, 10 mM dithiothreitol, 23 units reverse transcriptase (Anglian Biotec, Colchester, U.K.), 3.5 pmoles of the V_L region-specific oligonucleotide primer V_{K1}FOR [5'-d(GTT AGA TCT CCA GCT TGG TCC C)] or the V_H region-specific primer V_{H1}FOR-B [5,-d(TGA GGA GAC GGT GAC CGT GGT CCC TTG GCC)], and incubated for 5 minutes at 20°C and then 90 minutes at 42°C.

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Subsequent 50 μ l PCR amplifications consisted of 5 μ l of the first strand synthesis reaction (unpurified), 500 μ M each dNTP, 67 mM Tris-HCl (pH 8.8 at 25°C), 17 mM $(\text{NH}_4)_2\text{SO}_4$, 10 mM MgCl₂, 20 μ g/ml gelatin, 5 units TAQ DNA 5 polymerase (Koch-Light, Haverhill, U.K.), and 25 pmoles (each) of primers V_K1FOR and V_K1BACK [5'-d(GAC ATT CAG CTG ACC CAG TCT CCA)] for the V_L region or V_H1FOR-B and the mixed primer V_H1BACK [5'-d(AG GT(CG) (CA)A(GA) CTG CAG (GC)AG TC(TA) GG)] for the V_H region. Reactions were 10 overlayed with mineral oil and subjected to 30 cycles of 1.5 minutes at 95°C (denaturation), 1.5 minutes at 37°C (V_L) or 50°C (V_H; annealing), and 3 minutes at 72°C (extension) with a Techne PHC-1 programmable cyclic reactor. The final cycle contained a 10 minute extension 15 time.

The samples were frozen at -20°C and the mineral oil (a viscous liquid at -20°C) was removed by aspiration. The aqueous phases were thawed, and PCR products were purified by electrophoresis in 2% agarose gels, and then double 20 digested with either PvuII and BglII (V_L) or PstI and BstEII (V_H) restriction enzymes, and cloned into the PvuII and BcII restriction sites of the vector M13V_KPCR3 (for V_L region; Orlandi *et al*, 1989) or the PstI and BstEII restriction sites of the vector M13V_HPCR1 (for V_H region). 25 As described in the results, V_L region clones were first screened by hybridisation to a ³²P-labeled oligonucleotide probe [5'-d(GTT TCA TAA TAT TGG AGA CA)] specific for the CDR2 of the Y3-Ag 1.2.3 V_L region. V_L region clones not hybridising to this probe and V_H region clones were 30 sequenced by the dideoxy chain termination method (Sanger *et al*, PNAS USA 74: 5463, 1977).

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Reshaped Light Chain Variable Region and Expression Vector Construct.

The reshaped light chain was constructed by oligonucleotide-directed *in vitro* mutagenesis in an M13 vector by priming with three oligonucleotides simultaneously on a 748 base single-stranded cDNA template encoding the entire V_L and kappa constant (C_K) regions of the reshaped CAMPATH-1 antibody (Reichmann *et al.*, *Nature* 332: 323-327, 1988). The three oligonucleotides [5'-d(AGA GTG ACC ATC ACC TGT CTA GCA AGT GAG GAC ATT TAC AGT GAT TTA GCA TGG TAC CAG CAG AAG CCA), 5'-d(CTG CTG ATC TAC AAT ACA GAT ACC TTG CAA AAT GGT GTG CCA AGC AGA TTC), 5'-d(ATC GCC ACC TAC TAC TGC CAA CAG TAT AAC AAT TAT CCG TGG ACG TTC GGC CAA GGG ACC)] were designed to replace each of the three CDRs in the REI-based human antibody V_L region framework that is part of the reshaped CAMPATH-1 antibody V_L region (Reichmann *et al.*, 1988). A clone containing each of the three mutant oligonucleotides was identified by nucleotide sequencing and was subcloned into the HindIII site of the expression vector pH β APr-1 (Gunning *et al.*, *PNAS*, 84: 4831-4835, 1987) which also contained a dihydrofolate reductase gene (Ringold *et al.*, *J.Mol.Appl. Genet.* 1: 165-175, 1981) driven by a truncated SV40 promoter.

25 Reshaped Heavy Chain Variable Regions Based on the Variable Region Framework of the Human Antibody NEW, and Expression Vector Constructs.

Two versions of the NEW-based reshaped heavy chain were created, CD4V_HNEW-Thr³⁰ and CD4V_HNEW-Ser³⁰. The CD4V_HNEW-Thr³⁰ version (Figure 6) encodes a threonine residue at 30 position 30 while the CD4V_HNEW-Ser³⁰ version (Figure 7) encodes a Ser residue at position 30. As a matter of convenience, CD4V_HNEW-Thr³⁰ was created first by oligonucleotide-directed *in vitro* mutagenesis in the vector M13mp18 by priming with three oligonucleotides

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simultaneously on a 1467 base single-stranded cDNA template (Figure 5) encoding the entire heavy chain of the reshaped CAMPATH-1 antibody (Reichmann *et al*, 1988). The three oligonucleotides [5'-d(TCT GGC TTC ACC TTC ACC AAC TAT GGC 5 ATG GCC TGG GTG AGA CAG CCA CCT), 5'-d(GGT CTT GAG TGG ATT GGA ACC ATT AGT CAT GAT GGT AGT GAC ACT TAC TTT CGA GAC TCT GTG AAG GGG AGA GTG), 5'-d(GTC TAT TAT TGT GCA AGA CAA GGC ACT ATA GCT GGT ATA CGT CAC TGG GGT CAA GGC AGC CTC)] were designed to replace each of the three complementarity 10 determining regions (CDRs) in the NEW-based V_H region that is part of the reshaped CAMPATH-1 antibody (Reichmann *et al*, 1988). A clone (Figure 6) containing each of the three mutant oligonucleotides was identified by nucleotide sequencing. CD4 V_H NEW-Ser³⁰ was created second by 15 oligonucleotide-directed *in vitro* mutagenesis in the vector M13mp18 by priming with a single oligonucleotide on the 1458 base single-stranded cDNA template (Figure 6) encoding CD4 V_H NEW-Thr³⁰. The oligonucleotide [5'-d(GCT TCA CCT TCA GCA ACT ATG GCA T)] was designed to mutate the residue at 20 position 30 from threonine [ACC] to serine [AGC]. A clone (Figure 7) containing this mutant oligonucleotide was identified by nucleotide sequencing. Double-stranded forms of the clones CD4 V_H NEW-Thr³⁰ and CD4 V_H NEW-Ser³⁰ were subcloned as HindIII fragments into the HindIII site of the 25 expression vector pNH316. The vector pNH316 is a modified version of the vector pH β APr-1 (Gunning *et al*, PNAS, 84: 4831-4835, 1987) which was engineered to contain a neomycin resistance gene driven by a metallothioneine promoter.

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Reshaped Heavy Chain Variable Regions Based on the Variable Region Framework of the Human Antibody KOL, and Expression Vector Constructs

Two versions of the KOL-based reshaped heavy chain were created, CD4V_HKOL-Thr¹¹³ and CD4V_HKOL-Pro¹¹³. The CD4V_HKOL-Thr¹¹³ version encodes a threonine residue at position 113 (Figure 11) while the CD4V_HKOL-Pro¹¹³ version encodes a proline residue at position 113 (Figure 9). As a matter of convenience, CD4V_HKOL-Thr¹¹³ was created first by oligonucleotide-directed *in vitro* mutagenesis of single-stranded DNA template containing the 817 base HindIII-BamHI fragment encoding the V_H region of the rat CD4 antibody (Figure 4) cloned into M13mp18 by priming simultaneously with five oligonucleotides [5'-d(CAC TCC CAG GTC CAA CTG GTG GAG TCT GGT GGA GGC GTG GTG CAG CCT GG), 5'-d(AAG GTC CCT GAG ACT CTC CTG TTC CTC CTC TGG ATT CAT CTT CAG TAA CTA TGG CAT G), 5'-d(GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG), 5'-d(ACT ATC TCC AGA GAT AAT AGC AAA AAC ACC CTA TTC CTG CAA ATG G), 5'-d(ACA GTC TGA GGC CCG AGG ACA CGG GCG TGT ATT TCT GTG CAA GAC AAG GGA C)] which were designed to replace the rat framework regions with the human framework regions of KOL. A clone containing each of the five mutant oligonucleotides was identified by nucleotide sequencing. CD4V_HKOL-Pro¹¹³ was created second by oligonucleotide-directed *in vitro* mutagenesis of single-stranded DNA template containing the 817 base HindIII-BamHI fragment encoding CD4V_HKOL-Thr¹¹³ cloned into M13mp18 by priming with the oligonucleotide [5'-d(TGG GGC CAA GGG ACC CCC GTC ACC GTC TCC TCA)]. A clone containing this mutant oligonucleotide was identified by nucleotide sequencing. The immunoglobulin promoters were removed from the double-stranded DNA forms of clones encoding CD4V_HKOL-Thr¹¹³ (Figure 11) and CD4V_HKOL-Pro¹¹³ (Figure 9) by replacing (for both versions) the first 125 bp (HindIII-NcoI) with a HindIII-NcoI oligonucleotide linker fragment

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[5'-d(AGC TTT ACA GTT ACT GAG CAC ACA GGA CCT CAC) and its overlapping complement 5'-d(CAT GGT GAG GTC CTG TGT GCT CAG TAA CTG TAA)]. The resultant clones, CD4V_HKOL-Thr¹¹³ (Figure 12) and CD4V_HKOL-Pro¹¹³ (Figure 10), now 731 bp

5 HindIII-BamHI fragments, were separately subcloned into the HindIII and BamHI cloning sites of the expression vector pH β APr-1-gpt (Gunning *et al*, PNAS USA 76, 1373, 1987) into which had been cloned the human IgG1 constant region gene (Bruggemann *et al*, J.Exp.Med. 166, 1351-1361, 1987) at the

10 BamHI site. Thus, when transfected and expressed as antibody heavy chains (see below), these reshaped V_H regions are linked to human IgG1 constant regions.

Fluorescence activated cell sorter (FACS) analysis

The relative affinities of the reshaped antibodies to

15 bind the CD4 antigen were estimated by FACS analysis. The CD4-expressing cells used in this analysis were a cloned rat T cell line NB2-6TG stably transfected with an expression vector containing a complementary DNA (cDNA) encoding the human CD4 antigen (Maddon *et al*, Cell, 42, 93-104, 1985). Cells were stained with the appropriate

20 reshaped antibody followed by fluorescein-conjugated sheep anti-human antibodies (Binding Site Ltd., Birmingham, UK). Control staining (see Table 1) consisted of no antibody present during the first stage of cell staining. Mean

25 cellular fluorescence was determined with an Ortho FACS.

Antibody avidity analysis

The relative avidities of the rat YNB46.1.8 antibody and the reshaped CD4V_HKOL-Thr¹¹³ antibody were estimated by an enzyme-linked immunosorbent assay (ELISA). Microtiter

30 plates were coated with soluble recombinant CD4 antigen (Byrn *et al*, Nature, 344: 667-670, 1990) at 50 μ l/well, 10 μ g/ml, and then blocked with 100 μ l/well phosphate buffered saline (PBS) containing 1.0% bovine serum albumin

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(BSA). Antibodies were diluted in PBS containing 0.1% BSA, and added to wells (50 ul/well) for 45 minutes at room temperature. Biotinylated CD4V_HKOL-Thr113 antibody (10 ul/well; 20 ug/ml final concentration) was then added to 5 each well for an additional 45 minutes. Wells were washed with PBS containing 0.1% BSA, and then 50 ul streptavidin-biotinylated horseradish peroxidase complex (Amersham; Aylesbury, UK) diluted 1:1,000 was added to each well for 10 30 minutes. Wells were washed with PBS containing 0.1% BSA, and 100 ul substrate (25 mM citric acid, 50 mM disodium hydrogen phosphate, 0.1% (w/v) o-phenylene 15 diamine, 0.04% (v/v) 30% hydrogen peroxide) was added to each well. Reactions were stopped by the addition of 50 ul/well 1.0 M sulfuric acid. Optical densities at 492 nanometers (OD₄₉₂) were determined with an ELISA plate reader.

Transfections.

Dihydrofolate reductase deficient chinese hamster ovary (CHO^{DHFR-}) cells (10⁶/T-75 flask) were cotransfected as 20 described (Wigler *et al*, PNAS USA 76, 1373, 1979) with 9 μ g of heavy chain construct and 1 μ g of the light chain construct. Transfectants were selected in medium containing 5% dialysed foetal bovine serum for 2 to 3 weeks, and antibody-secreting clones were identified by 25 ELISAs of conditioned media. Antibody was concentrated and purified by protein-A Sepharose (Trade Mark) column chromatography.

2. RESULTS

Cloning of Light and Heavy Chain Variable Region cDNAs.

30 cDNAs encoding the V_L and V_H regions from CD4 antibody-secreting hybridoma cells were isolated by PCR using primers which amplify the segment of mRNA encoding the N-

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terminal region through to the J region (Orlandi *et al*, 1989). V_L and V_H region PCR products were subcloned into the M13-based vectors M13 V_K PCR3 and M13 V_H PCR1, respectively. Initial nucleotide sequence analysis of 5 random V_L region clones revealed that most of the cDNAs encoded the V_L region of the light chain expressed by the Y3-Ag 1.2.3 rat myeloma cell line (Crowe *et al*, Nucleic Acid Research, 17: 7992, 1989) that was used as the fusion partner to generate the anti-CD4 hybridoma. It is likely 10 that the expression of the Y3-Ag 1.2.3 light chain mRNA is greater than that of the CD4 antibody light chain, or the Y3-Ag 1.2.3 light chain mRNA is preferentially amplified 15 during the PCR.

To maximize the chance of finding CD4 V_L region cDNAs, 20 we first screened all M13 clones by hybridisation to a ^{32}P -labeled oligonucleotide probe that is complementary to the CDR 2 of Y3-Ag 1.2.3 (Crowe *et al*, Nucleic Acid Research, 17: 7992, 1989). Subsequent sequence analysis was 25 restricted to M13 clones which did not contain sequence complementary to this probe. In this manner, two cDNA clones from independent PCR amplifications were identified that encoded identical V_L regions. Nucleotide sequence analysis of random V_H region PCR products revealed a single species of V_H region cDNA. Two V_H cDNA clones from 30 independent PCR amplifications were found to contain identical sequences except that the codon of residue 14 encoded proline [CCT] in one clone while the second clone encoded leucine [CTT] at the same position.

According to Kabat *et al* 1987, 524 of 595 sequenced V_H 35 regions contain a proline residue at this position, while only 6 contain leucine. We have therefore chosen the proline-encoding clone for illustration (see below). As residue 14 lies well within the first V_H framework region and not in a CDR, it is unlikely to contribute directly to antigen binding, and the ambiguity at this position did not

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affect the subsequent reshaping strategy. Thus, we have not investigated this sequence ambiguity further.

The cDNA sequences and their predicted amino acid sequences are shown in Figures 1 and 4. As no additional 5 V_L or V_H region-encoding clones were found, it was assumed that these sequences were derived from the CD4 antibody genes.

Construction of reshaped antibodies.

Our goal was to investigate the importance of selecting 10 the appropriate human V region framework during reshaping. Two reshaping strategies were employed.

First reshaping strategy.

In the first strategy, we created a reshaped antibody that incorporated the CDRs from the rat-derived CD4 15 antibody and the same human V region framework sequences that we had previously successfully used for the reshaped CAMPATH-1 antibody, namely an REI-based framework for the V_L region and an NEW-based framework for the V_H region (Reichmann *et al.*, 1988). This was accomplished by 20 oligonucleotide-directed *in vitro* mutagenesis of the six CDRs of the reshaped CAMPATH-1 antibody light and heavy chain cDNAs shown in Figures 2 and 5, respectively. The resultant reshaped CD4 antibody light chain (Figure 3) is called CD4 V_L REI. Two versions of the NEW-based reshaped 25 CD4 antibody heavy chain were created: CD4 V_H NEW-Thr³⁰ (Figure 6) encoding a threonine residue at position 30 (in framework 1) and CD4 V_H NEW-Ser³⁰ (Figure 7) encoding a serine residue at position 30. These two different 30 versions were created because the successfully reshaped CAMPATH-1 antibody heavy chain bound antigen well whether position 30 encoded a threonine or serine residue

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(Reichmann *et al.*, 1988), and we chose to test both possibilities in this case as well.

Second reshaping strategy

In the second reshaping strategy, we have reshaped the 5 CD4 antibody V_H region to contain the V_H region framework sequences of the human antibody KOL. Of all known human antibody V_H regions, the overall amino acid sequence of the V_H region of KOL is most homologous to the rat CD4 antibody V_H region. The V_H regions of the human antibodies KOL and 10 NEW are 66% and 42% homologous to the rat CD4 antibody V_H region, respectively.

Two versions of the KOL-based reshaped CD4 antibody heavy chain V region were created that differ by a single amino acid residue within the fourth framework region: 15 CD4 V_H KOL-Pro¹¹³ (Figure 10) encodes a proline residue at position 113 and CD4 V_H KOL-Thr¹¹³ (Figure 12) encodes a threonine residue at position 113. CD4 V_H KOL-Pro¹¹³ is "true to form" in that its framework sequences are identical to those of the KOL antibody heavy chain V region 20 (Figure 8).

Of all known human antibody V_L regions, the overall amino acid sequence of the V_L region of the human light chain NEW is most homologous (67%) to the rat CD4 antibody V_L region. Thus, the identical reshaped light chain, 25 CD4 V_L REI (described above), that was expressed with the NEW-based reshaped CD4 antibody heavy chains CD4 V_H NEW-Thr³⁰ and CD4 V_H NEW-Ser³⁰, is also expressed with the KOL-based reshaped CD4 antibody heavy chains CD4 V_H KOL-Pro¹¹³ and CD4 V_H KOL-Thr¹¹³. This is advantageous because expression 30 of the same reshaped light chain with different reshaped heavy chains allows for a direct functional comparison of each reshaped heavy chain.

To summarise, four different reshaped antibodies were created. The reshaped light chain of each antibody is

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called CD4V_LREI. The reshaped heavy chains of the antibodies are called CD4V_HNEW-Thr³⁰, CD4V_HNEW-Ser³⁰, CD4V_HKOL-Pro¹¹³, and CD4V_HKOL-Thr¹¹³, respectively. Each of the reshaped heavy chains contain the same human IgG1 5 constant region. As each reshaped antibody contains the same reshaped light chain, the name of a reshaped antibody's heavy chain shall be used below to refer to the whole antibody (heavy and light chain combination).

Relative affinities of the reshaped antibodies

10 The relative affinities of the reshaped antibodies were approximated by measuring their ability to bind to CD4 antigen-expressing cells at various antibody concentrations. FACS analysis determined the mean cellular fluorescence of the stained cells (Table 1).

15 It is clear from this analysis that the reshaped CD4 antibodies bind to CD4 antigen to varying degrees over a broad concentration range. Consider Experiment 1 of Table 1 first. Comparing CD4V_HKOL-Thr¹¹³ antibody to CD4V_HNEW-Thr³⁰ antibody, it is clear that both antibodies bind CD4⁺ 20 cells when compared to the control, reshaped CAMPATH-1 antibody. However, CD4V_HKOL-Thr¹¹³ antibody binds CD4⁺ cells with far greater affinity than CD4V_HNEW-Thr³⁰ antibody. The lowest concentration of CD4V_HKOL-Thr¹¹³ antibody tested (2.5 ug/ml) gave a mean cellular 25 fluorescence nearly equivalent to that of the highest concentration of CD4V_HNEW-Thr³⁰ antibody tested (168 ug/ml). Experiment 2 demonstrates that CD4V_HNEW-Ser³⁰ antibody may bind CD4⁺ cells somewhat better than CD4V_HNEW-Thr³⁰. Only 2.5 ug/ml CD4V_HNEW-Ser³⁰ antibody is required 30 to give a mean cellular fluorescence nearly equivalent to 10 ug/ml CD4V_HNEW-Thr³⁰ antibody. Experiment 3 demonstrates that CD4V_HKOL-Thr¹¹³ antibody may bind CD4⁺ cells somewhat better than CD4V_HKOL-Pro¹¹³ antibody.

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From these assays, it is clear that the KOL-based reshaped antibodies are far superior to the NEW-based reshaped antibodies with regards to affinity towards CD4⁺ cells. Also, there is a lesser difference, if any, between 5 CD4V_HNEW-Thr³⁰ antibody and CD4V_HNEW-Ser³⁰ antibody, and likewise between CD4V_HKOL-Thr¹¹³ antibody and CD4V_HKOL-Pro¹¹³ antibody. A ranking of these reshaped antibodies can thus be derived based on their relative affinities for CD4⁺ cells:

10 CD4V_HKOL-Thr¹¹³ > CD4V_HKOL-Pro¹¹³ >> CD4V_HNEW-Ser³⁰ > CD4V_HNEW-Thr³⁰

It should be restated that each of the reshaped CD4 antibodies used in the above experiments have the identical heavy chain constant regions, and are associated with identical reshaped light chains. Thus observed differences 15 of binding to CD4⁺ cells must be due to differences in their heavy chain V regions.

Relative avidities of the rat YNB46.1.8 antibody and the reshaped CD4V_HKOL-Thr¹¹³ antibody

The relative avidities of the rat YNB46.1.8 antibody and 20 the reshaped CD4V_HKOL-Thr¹¹³ antibody were estimated by ELISA. In this assay, the ability of each antibody to inhibit the binding of biotinylated CD4V_HKOL-Thr¹¹³ antibody to soluble recombinant CD4 antigen was determined. Results of an experiment are shown in Figure 13. The 25 inhibition of binding of biotinylated CD4V_HKOL-Thr¹¹³ antibody was linear for both the unlabeled CD4V_HKOL-Thr¹¹³ and YNB46.1.8 antibodies near the optical density of 0.3. The concentrations of CD4V_HKOL-Thr¹¹³ and YNB46.1.8 30 antibodies that give an optical density of 0.3 are 28.7 and 1.56 ug/ml, respectively. Thus the avidity of the YNB46.1.8 antibody can be estimated to be 28.7/1.56 or about 18 times better than that of CD4V_HKOL-Thr¹¹³ antibody. It should be noted that this experiment only provides a rough approximation of relative avidities, not

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affinities. The rat YNB46.1.8 antibody contains a different constant region than that of the CD4V_HKOL-Thr¹¹³ antibody, and this could affect how well the antibodies bind CD4 antigen, irrespective of their actual affinities 5 for CD4 antigen. The actual affinity of the reshaped antibodies for CD4 antigen may be greater, lesser, or the same as the YNB46.1.8 antibody. The other reshaped antibodies CD4V_HKOL-Pro¹¹³, CD4V_HNEW-Ser³⁰, and CD4V_HNEW-Thr³⁰ have not yet been tested in this assay.

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Table 1. Mean cellular fluorescence of CD4⁺ cells
stained with reshaped antibodies

	<u>Reshaped Antibody</u>	<u>Concentration</u> (μ g/ml)	<u>Mean cellular Fluorescence</u>
5			
<u>Experiment 1.</u>			
	CD4V _H KOL-Thr ¹¹³	113	578.0
	CD4V _H KOL-Thr ¹¹³	40	549.0
	CD4V _H KOL-Thr ¹¹³	10	301.9
10	CD4V _H KOL-Thr ¹¹³	2.5	100.5
	CD4V _H NEW-Thr ³⁰	168	97.0
	CD4V _H NEW-Thr ³⁰	40	40.4
	CD4V _H NEW-Thr ³⁰	10	18.7
	CD4V _H NEW-Thr ³⁰	2.5	10.9
15	CAMPATH-1	100	11.6
	CAMPATH-1	40	9.4
	CAMPATH-1	10	9.0
	CAMPATH-1	2.5	8.6
	CONTROL	----	9.0
20	<u>Experiment 2.</u>		
	CD4V _H NEW-Thr ³⁰	168	151.3
	CD4V _H NEW-Thr ³⁰	40	81.5
	CD4V _H NEW-Thr ³⁰	10	51.0
	CD4V _H NEW-Thr ³⁰	2.5	39.3
25	CD4V _H NEW-Ser ³⁰	160	260.2
	CD4V _H NEW-Ser ³⁰	40	123.5
	CD4V _H NEW-Ser ³⁰	10	68.6
	CD4V _H NEW-Ser ³⁰	2.5	49.2
	CONTROL	----	35.8
30	<u>Experiment 3.</u>		
	CD4V _H KOL-Pro ¹¹³	100	594.9
	CD4V _H KOL-Pro ¹¹³	40	372.0
	CD4V _H KOL-Pro ¹¹³	10	137.7
	CD4V _H KOL-Pro ¹¹³	2.5	48.9
35	CD4V _H KOL-Thr ¹¹³	100	696.7
	CD4V _H KOL-Thr ¹¹³	40	631.5
	CD4V _H KOL-Thr ¹¹³	10	304.1
	CD4V _H KOL-Thr ¹¹³	2.5	104.0
	CONTROL	----	12.3

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CLAIMS

1. A process for the preparation of an antibody chain in which the complementarity determining regions (CDRs) of the variable domain of the antibody chain are derived from a first mammalian species and the framework of the variable domain and, if present, the or each constant domain of the antibody chain are derived from a second different mammalian species, which process comprises:
 - (i) mutating the framework-encoding regions of DNA encoding a variable domain of an antibody chain of the said first species such that the mutated framework-encoding regions encode the said framework derived from the said second species; and
 - (ii) expressing the said antibody chain utilising the mutated DNA from step (i).
2. A process according to claim 1, wherein the framework-encoding regions of DNA encoding the variable domain of an antibody heavy chain are mutated in step (i).
3. A process according to claim 1 or 2, wherein the framework-encoding regions of DNA encoding the variable domain of an antibody light chain are mutated in step (i).
4. A process according to any one of the preceding claims, wherein the said first species is rat or mouse.
5. A process according to any one of the preceding claims, wherein the said second species is human.
6. A process according to any one of the preceding claims, comprising:

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(a) determining the nucleotide and predicted amino acid sequence of a variable domain of a selected antibody chain of the said first species;

5 (b) determining the antibody framework to which the framework of the said domain is to be altered;

(c) mutating the framework-encoding regions of DNA encoding the said variable domain such that the mutated framework-encoding regions encode the framework determined upon in step (b).

10 (d) linking the mutated DNA obtained in step (c) to DNA encoding a constant domain of the said second species and cloning the DNA into an expression vector; and

(e) introducing the expression vector into a compatible host cell and culturing the host cell under such 15 conditions that antibody chain is expressed.

7. A process according to claim 6, in which about the most homologous framework of an antibody chain of a different species is selected in step (b) as the framework to which the framework of the said variable domain is to be 20 altered.

8. A process according to any one of the preceding claims, wherein the antibody of the said first species is a CD4 antibody.

9. A process according to any one of the 25 preceding claims, wherein the said antibody chain is co-expressed with a complementary antibody chain and antibody comprising the said two chains is recovered.

10. An antibody which is capable of binding to human CD4 antigen, in which the CDRs of the light chain of 30 the antibody have the amino acid sequences:

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CDR1: LASEDIYSDLA
CDR2: NTDTLQN
CDR3: QQYNNYPWT

in which the CDRs of the heavy chain of the antibody have
5 the amino acid sequences:

CDR1: NYGMA
CDR2: TISHDGSDTYFRDSVKG
CDR3: QGTIAGIRH, and

in which the framework of the variable domain and, if
10 present, the or each constant domain of each chain are
derived from a mammalian non-rat species.

11. An antibody according to claim 10, in which
the mammalian non-rat species is human.

12. An antibody according to claim 11, in which
15 the variable domain framework of the heavy chain is
homologous to the heavy chain variable domain framework of
the protein KOL.

13. An antibody according to claim 12, in which
the heavy chain variable region has the amino acid sequence
20 shown in the upper line in Figure 10 or 12.

14. An antibody according to claim 11, in which
the variable domain framework of the heavy chain is
homologous to the heavy chain variable domain framework of
the protein NEW.

25 15. An antibody according to claim 14, in which
the heavy chain variable region has the amino acid sequence
shown in the upper line of Figure 6 or 7.

16. An antibody according to any one of claims 11
to 15, in which the variable domain framework of the light

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chain is homologous to the variable domain framework of the protein REI.

17. An antibody according to claim 16, in which the light chain has the amino acid sequence shown in the 5 upper line of Figure 3.

18. A pharmaceutical composition comprising a pharmaceutically acceptable carrier or diluent and, as active ingredient, an antibody as claimed in any one of claims 10 to 17.

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FIG. 1

HindIII

1 AAGCTTATGAAATATGCAAATCCTCTGAATCTACATGGTAATATAGGTTTGTCTATAACC 59

60 ACAAACAGAAAAACATGAGATCACAGTTCTCTACAGTTACTGAGCACACAGGACCTCA 119

-19 M G W S C I I L F L V A T A T -5

120 CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGGTACAGGCTAAGGGGTGCA 179

180 CAGTAGCAGGCCTTGAGGTCTGGACATATATGGGTGACAATGACATCCACCTTGCCRTT 239

-4 G V H S D I Q L T Q S P V S L S A 13

240 CTCTCCACAGGTGTCCACTCCGACATCCAGCTGACCCAGTCAGTCTCCAGTTCTGTCTGCA 299

CDR1

14 S L G E T V N I E C L A S E D I Y S D L 33

300 TCTCTGGGAGAAACTGTCAACATCGAATGTCTAGCAAGTGAAGGACATTACAGTGATTAA 359

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FIG. 1 (contd.)

34	<u>A</u>	W	Y	Q	Q	K	P	G	K	S	P	Q	L	L	I	Y	CDR 2		
360	GCATGGTATCAGCAGAAGCCAGGGAAATCTCCTCAACTCCTGATCTATAATAACAGATAACC															419			
54	<u>L</u>	Q	N	G	V	P	S	R	F	S	G	S	G	T	Q	Y	S	L	73
420	TTGCAAAATGGGGTCCCTTCACGGTTAGTGGCAGTGGATCTGGCACACAGTATTCTCTA															479			
74	K	I	N	S	L	Q	S	E	D	V	A	T	Y	F	C	CDR 3			
480	AAAATAAACAGCCTGCCAAATCTGAAGATGTCGCAACTTCTGTCAACAAATAACAAAT															539			
94	<u>Y</u>	P	W	T	F	G	G	G	T	K	L	E	I	K	R	CDR 3			
540	TATCCCGTGGACGTTCTGGAGGGACCAAGCTGGAGATCAAACCGTAGAATTAAAC															599			
600	TTTGCTTCCTCAGTGGATCC															620			

BamHI

FIG. 2

-19 1 HindIII AACCTTC

-19	HindIII	M G W S C I	-14
1	AAGCTTGGCTTACAGTTACTGAGCACACGGACCTCACCATGGGATGGAGCTGTATC	58	
-13	I L F L V A T A T G V H S D I Q M T Q S	7	
59	ATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCCGACATCCAGATGACCCAGGC	118	
	CDR 1		
8	P S S L S A S V G D R V T I T C	27	
119	CCAAGCAGGCCAGCGTGGGTGACAGAGTGAACCATCACCTGAAAGCAAAGTCAG	178	
28	N I D K Y L N W Y Q Q K P G K A P K L L	47	
179	AATATTGACAAATACTTAAACTGGTACCGGCCAGGAAGGCTAAAGGCTCCAAAGCTGCTG	238	
	CDR 2		
48	I Y N T N N L Q T G V P S R F S G S G S	67	
239	ATCTACAATAACAAATTGCAAACGGGTGTGCCAAGCAGATTCAGCGGTAGCGGTAGC	298	
68	G T D F T F T I S S L Q P E D I A T Y Y	87	
299	GGTACCGACTTCACTTCACCATCAGCAGCCAGGACATGCCACCTACTAC	358	

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FIG. 2 (contd.)

CDR 3												
88	C	L	Q	H	I	S	R	P	R	T	F	
359	TGCTTGAGGATATAAGTAGGCCGGCACGGTTCGGCAAGGAAATCAAA											107
108	R	T	V	A	A	P	S	V	F	I	F	
419	CGAACTGGCTGGCACCATCTGCTCATCTGCCATCTGATGAGCAGTTGAAATCT											127
128	G	T	A	S	V	V	C	L	L	N	N	
479	GGAACTGCCTCTGTGTTGCTGCTGCTGAATAACTTCTATCCCAGAGGCCAAAGTACAG											147
148	W	K	V	D	N	A	L	Q	S	G	N	
539	TGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGACTGTCAACAGAGCAGGAC											538
168	S	K	D	S	T	Y	S	L	S	T	L	
599	AGCAAGGACACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCACTACAG											167
188	K	H	K	V	Y	A	C	E	V	T	H	
659	AAACACAAAGTCTACGGCTGGAAAGTCACCCATCAGGGCCTGAGCTGGCCGTACAAG											187
208	S	F	N	R	G	E	C	T	m	HindIII	214	
719	AGCTTCAACAGGGAGAGTGTAGAAGCT											748

FIG. 3

-19 *Hind* III M G W S C I -14
 1 AAGCTTGGCTTACAGTTACTGAGCACACAGGACCTCACCATGGGATGGAGCTGTATC 58
 -13 I L F L V A T A T G V H S D I Q M T Q S 7
 59 ATCCTCTTGGTAGCAAACAGCTACAGGTGTTCCACTCCGACATCCAGATGACCCAGAGC 118
 8 P S S L S A S V G D R V T I T C L A S E 27
 119 CCAAGCAGCCTGAGCGGCCAGGGTGGGTGACAGAGTGAACCATCACCTGAGCAAGTGAG 178
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 28 D I Y S D L A W Y Q Q K P G K A P K L L 47
 179 GACATTACAGTGATTAGCATGGTACCCAGCAGGAAGCCAGGTAAGGCTCCAAAGCTGCTG 238
 CDR 2
 48 I Y N T D T L Q N G V P S R F S G S G S 67
 239 ATCTACAATAACAGATAACCTTGCAAATGGTGTGCCAAGCAGATTCAAGGGTAGCCGGTAGC 298
 68 G T D F T F T I S S L Q P E D I A T Y Y 87
 299 GGTACCGACTTCACCTTCAACCATCAGCAGGCTCCAGCCAGGGACATGCCACCTACTAC 358
 CDR 3
 88 C Q Q Y N N Y P W T F G Q G T K V E I K 107
 359 TGCCAACAGTATAACAAATTATCCGGTGGACGTTGGCCAAGGGACCAAGGTGGAAATCAA 418

FIG. 3 (contd.)

108	R	T	V	A	A	P	S	V	F	I	F	P	P	S	D	E	Q	L	K	S	127				
419	CGAACTGTGGCTGCACCATCTGTCTTCATCTCCGCCATCTGAGCAGTTGAAATCT																				478				
128	G	T	A	S	V	V	C	L	L	N	N	F	Y	P	R	E	A	K	V	Q	147				
479	GGAACTGCCCTCTGTGTGCTGCTGAATAACTTCTATCCCAGAGGCCAAAGTACAG																				538				
148	W	K	V	D	N	A	L	Q	S	G	N	S	Q	E	S	V	T	E	Q	D	167				
539	TGGAAGGTGATAAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCCGAC																				598				
168	S	K	D	S	T	Y	S	L	S	S	T	L	T	L	S	K	A	D	Y	E	187				
599	AGCAAGGACACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAG																				658				
188	K	H	K	V	Y	A	C	E	V	T	H	Q	G	L	S	S	P	V	T	K	207				
659	AACACAAAGTCTACGGCTGCGAAGTCACCCATCAGGGCCTGAGCTGCCCCGTACAAAG																				718				
208	S	F	N	R	G	E	C	Trm	HindIII																214
719	AGCTTCAACAGGGAGAGTGTAGAAGCTT																				748				

FIG. 4

HindIII

1	AAGCTTATGCAAATCCTCTGAATCTACATGGTAAATATAAGTTTGTCTATAACC	59
60	ACAAACAGAAAAACATGAGATCACAGTTCTACAGTTACTCAGCACACAGGACCTCA	119
-19	M G W S C I I L F L V A T A T	-5
120	CCATGGGATGGAGCTGTATCATCCTCTTGGTAGCAACAGCTACAGGTAAAGGGCTCA	179
180	CAGTAGCCAGGCTTGAGGTGACATATATGGGTGACAATGACATCCACTTGCCTT	239
-4	G V H S Q V Q L Q E S G G G L V Q	13
240	CTCTCCACAGGTGTCCACTCCCAGGTCCAACACTGCAGGAGTCTGGAGGCTTAGTGCAG	299
14	P G R S L K L S C A A S G L T F S <u>N Y G</u>	33
300	CCTGGAAGGTCCCTGAAACTCTCCCTGTGCAGGCCTCTGGACTCACTTTCACTAACTATGGC	359
34	<u>M A</u> W V R Q A P T K G L E W V A <u>T I S H</u>	53
360	<u>ATGGCCTGGGTCCGCCAGGCTCCAACGAAGGGCTGGAGGTGGCTCGCAACCATTAGTCAT</u>	419

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FIG. 4 (contd.)

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FIG. 5

-19	<i>Hind</i> III	M	G	W	S	C	I	I	L	-12											
1	AAGCTTACAGTTACTGAGCACACAGGACCTCACCATGGATGGCTGAGCTGATCATCCTC									59											
-11	F	L	V	A	T	G	V	H	S	Q	9										
60	TTCTTGGTAGCAACAGCTACAGGTGTCACACTCCCAGGTCCAACTGCAGGAGGGTCCA									119											
10	G	L	V	R	P	S	Q	T	L	S	29										
120	GGTCTTGTGAGACCTAGCCAGACCCCTGACCTGAGCCTGACCTGCACCGTGTCTGGCTCACCTTC										179										
	CDR 1																				
30	T	D	F	Y	M	N	W	V	R	Q	P	P	G	R	G	L	E	W	I	F	49
180	ACCGATTCTACATGAACTGGGTGAGACAGCCACCTGGACAGGCTTGAGTGGATTGGA																				239
	CDR 2																				
50	F	I	R	D	K	A	K	G	Y	T	T	E	Y	N	P	S	V	K	G	R	69
240	TTTATAGAGACAAGCTAAAGGTTACACAAACAGAGTACAATCCATCTGTGAAGGGAGA																				299

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FIG. 5 (contd.)

70	V	T	M	L	V	D	T	S	K	N	Q	F	S	L	R	L	S	S	V	T	89
300	GTGACAATGCTGGTAGACACCAGCAAGAACCGTTCAGGCCTCAGGCTGAGACTCAGCAGCGTGACA																				359
90	A	A	D	T	A	V	Y	Y	C	A	R	E G H T A A P F D					109				
360	<u>GCCGCCGACACCGGGGTCTTATTGTGCAAGAGAGGGCCACACTGCTCCCTTTGAT</u>																				419
110	<u>Y</u>	W	G	Q	G	S	L	V	T	V	S	S	A	S	T	K	G	P	S	V	129
420	TACTGGGTCAAGGCAGGCCCTCGTCACAGTCTCCTCAGGCTCCACCAAGGGCCCATCGGTC																				479
130	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L	G	C	L	149
480	<u>TTCCCCCTGGCACCCCTCCCAAGAGCACCCACTCTGGGGCACAGGGCCCTGGGCTGCCCTG</u>																				539
150	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S	G	A	L	T	S	169
540	GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGACTCAGGGCCCTGACCCAGC																				599

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FIG. 5 (contd.)

170	G	V	H	T	F	P	A	V	L	Q	S	S	G	L	Y	S	L	S	S	V	189
600	GGCGTGCACACCTTCCCCGGCTGTCCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTG																			659	
190	V	T	V	P	S	S	L	G	T	Q	T	Y	I	C	N	V	N	H	K	209	
660	GTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTCAGTCAACAG																			719	
210	P	S	N	T	K	V	D	K	K	V	E	P	K	S	C	D	K	T	H	T	229
720	CCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCCAAATCTTGTGACAAAACCTCACACA																			779	
230	C	P	P	C	P	A	P	E	L	L	G	G	P	S	V	F	L	F	P	P	249
780	TGGCCACCGTCCCCAGCACCTGAACTCCCTGGGGGACCCGTCAAGTCTTCCTCTCCCCCA																			839	
250	K	P	K	D	T	L	M	I	S	R	T	P	E	V	T	C	V	V	D	269	
840	AAACCCAAAGGACACCCCTCATGATCTCCCCGACCCCTGAGGTACATGGCTGGTGGAC																			899	

FIG. 5 (contd.)

270	V	S	H	E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	289
900	GTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAT																			959	
290	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S	V	309
960	AATGCCAAGACAAAGCCGGGGAGGAGCAGTACAACAGCACCGTACCGTGTGGTCAGCGTC																			1019	
310	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K	V	S	N	329
1020	CTCACCGTCCCTGGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCTCCAAC																			1079	
330	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K	G	Q	P	R	E	349
1080	AAAGCCCTCCCAGCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA																			1139	
350	P	Q	V	Y	T	L	P	P	S	R	D	E	L	T	K	N	Q	V	S	L	369
1140	CCACAGGTGTACACCCCTGGCCCATCCCCATGGAGCTGACCAAGAACCAAGGCTGAGCCTG																			1199	

FIG. 5 (contd.)

370 T C L V K G F Y P S D I A V E W E S N G 389
 1200 ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGACTGGAGAGCAATGGG 1259
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390 Q P E N N Y K T T P P V L D S D G S F F 409
 1260 CAGCCGGAGAACAACTACAAGACCAACCGCCTCCGTGGACTCCGACGGCTCCTTCATTC 1319

410 L Y S K L T V D K S R W Q Q G N V F S C 429
 1320 CTCTACAGCAAGGCTCACCGTGGACAAGAGCAGGTGGCAGGGAAACGCTCTCATGCC 1379

430 S V M H E A L H N H Y T Q K S L S L S P 448
 1380 TCCGTGATGGCATGAGGCTCTGCACAAACCACTACACGCCAGAAGAGCCTCTGTCTCCCG 1439

449 G K Trm HindIII 450
 1440 GGTAAATGAGTGGCGACGGCCCCAAGCTT 1467

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FIG. 6

-19	HindIII	M	G	W	S	C	I	I	L	-12											
1	AAGCTTACAGTTACTGAGCACACAGGACCTCACCATGGGATGGCTATCATCCCTC									59											
-11	F	L	V	A	T	G	V	H	S	Q	V	Q	L	Q	E	S	G	P	9		
60	TTCTTGGTAGCAACAGGCTACAGGTGTCACACTCCCAGGTCCAACTGCAGGAGGGTCCA																			119	
10	G	L	V	R	P	S	Q	T	L	S	L	T	C	T	V	S	G	F	T	F	29
120	GGTCTTGTGAGACCTAGCCAGACCCTGACCTGAGCCCTGAGCTGCACCGTGTCTGGCTTCACCTTC																				179
	CDR 1																				
30	T	N	Y	G	M	A	W	V	R	Q	P	P	G	R	G	L	E	W	I	G	49
180	ACCAACTATGGCATGGCCTGGGTGAGACAGCCACCTGGACCGAGGTCTTGACTGGATTGGA																				239
	CDR 2																				
50	T	I	S	H	D	G	S	D	T	Y	F	R	D	S	V	K	G	R	V	T	69
240	ACCATTAGTCATGATGGTAGTGCACACTTACTTTGAGACTCTGTGAAGGGAGAGTGACAA																				299

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FIG. 6 (contd.)

70	M	L	V	D	T	S	K	N	Q	F	S	L	R	L	S	S	V	T	A	A	89
300	ATGCTGGTAGACACCAGCAAGAACCAAGCTCAGCCTGAGACTCAGCAGCGTGACAGGCCGCC																			359	
	CDR 3																				
90	D	T	A	V	Y	C	A	R	<u>Q</u>	<u>G</u>	<u>T</u>	<u>I</u>	<u>A</u>	<u>G</u>	<u>I</u>	<u>R</u>	<u>H</u>	W	G	109	
360	GACACCGGGGTCTATTATTGTGCAAGACAAGGCACATATAAGCTGGTATAACGTCACTGGGGT																			419	
110	Q	G	S	L	V	T	V	S	S	A	S	T	K	G	P	S	V	F	P	L	129
420	CAAGGCAGGCCCTCGTCACAGTCTCCTCAGGCCACCAAGGGCCCATCGGTCTTCCCGCTG																			479	
130	A	P	S	S	K	S	T	S	G	G	T	A	A	L	G	C	L	V	K	D	149
480	GCACCCCTCCCAAGAGCACCTCTGGGGCACAGGGCCCTGGCTGGTCAAGGAC																			539	
150	Y	F	P	E	P	V	T	V	S	W	N	S	G	A	L	T	S	G	V	H	169
540	TACTTCCCCGAACCCGGTGACGGGTGAACTCAGGGCCCTGACCCAGGGGGCAC																			599	

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FIG. 6 (contd.)

170	T	F	P	A	V	L	Q	S	S	G	L	Y	S	L	S	S	V	V	T	V	189
600	ACCTTCCGGCTGTCCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTG																			659	
190	P	S	S	S	L	G	T	Q	T	Y	I	C	N	V	N	H	K	P	S	N	209
660	CCCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAACCGTGAATCACAAAGCCAGCAAC																			719	
210	T	K	V	D	K	V	E	P	K	S	C	D	K	T	H	T	C	P	P	229	
720	ACCAAGGTGACAAGAAAGTTGAGCCCAAAATCTTGTGACAAAACATCACACATGCCACCG																			779	
230	C	P	A	P	E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	249
780	TGCCCAAGCACCTGAAACTCCCTGGGGGACCGCTCAGTCTTCTCTCTTCCCCAAACCCAAAG																			839	
250	D	T	L	M	I	S	R	T	P	E	V	T	C	V	V	D	V	S	H	269	
840	GACACCCTCATGATCTCCGGACCCCTGAGGTCACATGCCGTGGTGGACGTGAGCCAC																			899	

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FIG. 6 (contd.)

270	E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N	A	K	289
900	GAAGACCCCTGAGGTCAAGTTCAACTGGTACACTGGACCGGGTGGAGGTGCGATAATGCCAAG	959																			
290	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S	V	L	T	V	309
960	ACAAAGCCGGGGAGGAGGCAACTACAGCACGTACCCGTGTGGTCAGCGTCCCTCACCGTC	1019																			
310	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K	V	S	N	K	A	L	329
1020	CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCACAAAGGTCTCCAAACAAAGCCCTC	1079																			
330	P	A	P	I	E	K	T	I	S	K	A	K	G	Q	P	R	E	P	Q	V	349
1080	CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACAGGTG	1139																			
350	Y	T	L	P	P	S	R	D	E	L	T	K	N	Q	V	S	L	T	C	L	369
1140	TACACCCCTGCCCCCATCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACCTGCCCTG	1199																			

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FIG. 6 (contd.)

370	V	K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N	G	Q	P	E	389
1200	GTCAAAGGCTTCTATCCCAGCGACATGCCGTGGACTGGAGAGCAATGGGCAGCCGGAG																			1259	
390	N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S	F	F	L	Y	S	409
1260	AACAACTACAAAGACCAACGGCTTCCCGTGGACTCCGACGGCTCCCTCTACAGC																			1319	
410	K	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	429
1320	AAGCTCACCGTGGACAAGAGCAGGTGGCACAGGGAACGGTCTCATGCTCCGTGATG																			1379	
430	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	P	G	K	Trm		448	
1380	CATGAGGCTCTGCACAAACCAACTACACGGCAGAAGAGCCTCTCCCTGTCTCCGGTAAATGA																			1439	
<i>Hind</i> III																					
1440	GTGGCGACGGCCCCAAGGCT																			1458	

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FIG. 7

-19	<i>Hind</i> III	M	G	W	S	C	I	I	L	-12											
1	AAGCTTACAGTTACTGAGCACACGGACCTCACCATGGATGGCTATGTATCATCCTC									59											
-11	F	L	V	A	T	G	V	H	S	Q	V	Q	L	Q	E	S	G	P	9		
60	TTCTTGGTAGCAACAGCTAACAGGTCTACAGGTCCACTCCCAGGTCCAACTGCAGGAGAGCCGTC																			119	
10	G	L	V	R	P	S	Q	T	L	S	L	T	C	T	V	S	G	F	T	F	29
120	GGTCTTGTGAGACCTAGCCAGACCCCTGAGCTGACCTGCACCGTGTCTGCTCACCTTC																				179
30	S	N	Y	G	M	A	W	V	R	Q	P	P	G	R	G	L	E	W	I	G	49
180	AGCAACTATGGCATGGCCTGGGTGAGACAGCCACCTGGACAGGGTCTTGACTGGATTGGA																				239
50	T	I	S	H	D	G	S	D	T	Y	F	R	D	S	V	K	G	R	V	T	69
240	ACCATTAGTCATGATGGTAGTGTGACACTTACCTTCAAGGGAGAGTGACACTCTGTGAAGGGAGAGTGACAG																				299

CDR 1

CDR 2

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FIG. 7 (contd.)

70	M	L	V	D	T	S	K	N	Q	F	S	L	R	L	S	S	V	T	A	A	89
300	ATGCTGGTAGACACCAAGAACCGTTCAAGCCTGAGACTCAGCAGCGTGACAGGCC																			359	
	CDR 3																				
90	D	T	A	V	Y	C	A	R	<u>Q</u>	<u>G</u>	<u>T</u>	<u>I</u>	<u>A</u>	<u>G</u>	<u>I</u>	<u>R</u>	<u>H</u>	W	G	109	
360	GACACCGGGCTTATTATTGTGCAAGAACAGGCACTATAGCTGGTATAACGTCACTGGGT																			419	
110	Q	G	S	L	V	T	V	S	S	A	S	T	K	G	P	S	V	F	P	L	129
420	CAAGGCCAGCCTCGTCACACAGTCCTCAGCCTCCACCAAGGCCCATGGTCTTCCCCCTG																			479	
130	A	P	S	S	K	S	T	S	G	G	T	A	A	L	G	C	L	V	K	D	149
480	GCACCCCTCCTCCAAGAACCCACCTCTGGGGCACAGCGGCCCTGGCTGGTCAAGGAC																			539	
150	Y	F	P	E	P	V	T	V	S	W	N	S	G	A	L	T	S	G	V	H	169
540	TACTTCCCCGAAACCGGGTGAACGGTGTGGAACTCAGGGCCCTGACCAGGGCGTGGCAC																			599	

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FIG. 7 (contd.)

170	T	F	P	A	V	L	Q	S	G	L	Y	S	L	S	V	V	T	V	189		
600	ACCTTCCGGCTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGGTGGTACCGTG																	659			
190	P	S	S	S	L	G	T	Q	T	Y	I	C	N	V	N	H	K	P	S	N	209
660	CCCTCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACACACATGCCAAC																	719			
210	T	K	V	D	K	V	E	P	K	S	C	D	X	T	H	T	C	P	P	229	
720	ACCAAGGGACAAGAAAGTTGAGCCAAATCTTGTGACAAAACCTCACACATGCCACCG																	779			
230	C	P	A	P	E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	249
780	TGCCCCAGGACACTGAACCTCCGGGGGACCCGTCAGTCTTCCCTTCCCTTCCCTTCC																	839			
250	D	T	L	M	I	S	R	T	P	E	V	T	C	V	V	D	V	S	H	269	
840	GACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCCGTGGTACGTGAGGCCAC																	899			

FIG. 7 (contd.)

270	E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N	A	K	289
900	GAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG																			959	
290	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S	V	L	T	V	309
960	ACAAAGCCCCGGAGGAGCAGTACAACAGCACCGTACCGTACAGGACTGGCTGAATGGCAAGGAGTACAAGTGC																			1019	
310	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K	V	S	N	K	A	L	329
1020	CTGCACCGAGACTGGCTGAATGGCAAGGAGTACAAGTGC																			1079	
330	P	A	P	I	E	K	T	I	S	K	A	K	G	Q	P	R	E	P	Q	V	349
1080	CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGGAACCACAGGTG																			1139	
350	Y	T	L	P	P	S	R	D	E	L	T	K	N	Q	V	S	L	T	C	L	369
1140	TACACCCCTGCCCATCCCCGATGAGCTGACCAAGAACCGAGTCAAGCCTGACTGCC																			1199	

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FIG. 7 (contd.)

370	V	K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N	G	Q	P	E	389
1200	GTCAAAGGCTTCTATCCCAGCGACATGCCGTGGAGTGGAGAGCAATGGGCAGCCGGAG																				1259
390	N	N	Y	K	T	T	P	P	V	L	D	G	S	F	F	L	Y	S	409		
1260	AACAACTACAAGACACACGGCCTCCCGTGGACTCCGACGGCTCCTCTACAGC																				1319
410	K	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	429
1320	AAGCTCACCGTGGACAAGAGCAGGTGGCAGGGAAACGTCTCATGCTCCGTGATG																				1379
430	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P	G	K	Trm	448
1380	CATGAGGCTCTGGCACCAACCTACACGAGCAAGGAGGCTCTCCGTCTCCGTAAATGA																				1439
1440	<i>Hind</i> III																				1458

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FIG.8

1	Q	V	Q	L	V	E	S	G	G	G	V	V	Q	13							
14	P	G	R	S	L	R	L	S	C	S	S	S	G	CDR 1							
34	<u>M</u>	<u>Y</u>	W	V	R	Q	A	P	G	K	G	L	E	CDR 2							
54	D	G	S	D	Q	H	Y	A	D	S	V	K	G	CDR 3							
74	N	S	K	N	T	L	F	L	Q	M	D	S	L	R	P	E	D	T	G	V	93
94	Y	F	C	A	R	<u>D</u>	<u>G</u>	<u>G</u>	<u>H</u>	<u>G</u>	<u>F</u>	<u>C</u>	<u>S</u>	<u>S</u>	<u>A</u>	<u>S</u>	<u>C</u>	<u>F</u>	<u>G</u>	<u>P</u>	113
114	<u>D</u>	<u>Y</u>	W	Y	G	Q	G	T	P	V	T	V	S	S							126

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FIG. 9

HindIII

1	AAGCTTATGCAAATCCTCTGAATCTACATGGTAAATATAAGTTGTCTATAACC	59
60	ACAAACAGAAAAACATGAGATCACAGTTCTACAGTTACTCAGCACACAGGACCTCA	119
-19	M G W S C I I L F L V A T A T	-5
120	CCATGGATGGAGCTGTATCATCCCTCTGGTAGCAACAGCTACAGGTAAAGGGCTCA	179
180	CACTAGCAGGCTTCAAGGTCTGGACATATATGGTGACAATGACATCCACTTGCCTT	239
-4	G V H S Q V Q L V E S G G G V V Q	13
240	CTCTCCACAGGTGTCCACTCCAGGTCCAACTGGTGGAGTCTGGAGGGCTGGCAG	299
14	P G R S L R L S C S S S G F I F S	CDR1
300	CCTGGAAGGTCCCTGAGACTCTCCCTCTGGATTCACTCTTCACTAACTATGGC	359
34	<u>M A</u> W V R Q A P G K G L E W V A	CDR2
360	ATGGCCTGGTCCGGCCAGGCTCCAGGCAAGGGCTGGAGTGGTGGCAACCATTAGTCAT	419

FIG. 9 (contd.)

54	D	G	S	D	T	Y	F	R	D	S	V	K	G	R	F	T	I	S	R	D	73
420	GATGGTAGCTGACACTTACTTACTTTCGAGACTCCCGTGAAGGGCCGATTCACTATCTCCAGAGAT																			479	
74	N	S	K	N	T	L	F	L	Q	M	D	S	L	R	P	E	D	T	G	V	93
480	AATAGCAAAACACCCATTTCCTGCAAATGGACAGTCTGAGGCCCGAGGACACGGCCGTG																			539	
94	Y	F	C	A	R	Q	G	T	I	A	G	I	R	H	W	G	Q	G	T	P	113
540	TATTCTCTGCAAGACAAGGGACTATAGCAGGTATAACGTCACTGGGGCCAAGGGACCCCC																			599	
114	V	T	V	S	S																118
600	GTCACCCGCTCCTCAGGTGAGTCCTTACAACCTCTCTTCTATTCAAGCTAAATAGATT																			659	
660	TTACCTGCATTGTTGGGGAAATGTGTGTATCTGAATTTCAGGTCAATGAAGGACTAGG																			719	
720	GACACCTTGGAGTCAGAAAGGTCAATTGGGAGCCCCGGCTGATGCCAGACAGACATCCCTC																			779	
780	AGCTCCCAGACTTCATGGCCAGAGATTAGGGATCC																				
																				BamHI	
																				817	

FIG. 10

-19	<i>Hind</i> III	M G W S C I I L F	-11
1	AAGCTTACAGTTACTCAGCACACAGGACCTCACCATGGATGGCTATCATCCTCT		60
-10	L V A T A T		-5
61	TCTTGGTAGCAACAGGCTACAGGTAAAGGGCTCACAGTAGGCAGGCTTGAGGTCTGGACATA		120
-4		G V H S Q V	2
121	TATATGGGTGACAATGACATCCACCTTGCCTTCTCTCCACAGGTGTCACACTCCCCAGGTC		27/33
3	Q L V E S G G V V Q P G R S L R L S C		22
181	CAACTGGTAGTCTGGTGGAGGGCTGGCAGCCCTGGAAAGGTCCCTGAGACTCTCCTGT		180
	CDR 1		240
23	S S S G F I F S [N Y G M A] W V R Q A P G		42
241	TCCTCCTCTGGATTCACTCTCAGTAACATGGCATGGCTGGGCTGGGCTCCAGGCC		300
	CDR 2		
43	K G L E W V A [T I S H D G S D T Y F R D		62
301	AAGGGCTGGAGTGGTGGCAACCATAGTCATGATGGTAGTGCACACTTACTTCGAGAC		360

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FIG. 10 (contd.)

63	S	V	K	G	R	F	T	I	S	R	D	N	S	K	N	T	L	F	L	Q	82
361	<u>TCCGTGAAGGGCCGATTCACTATCTCCAGAGATAATAGCAAAACACCATTCTGCAA</u>																				420
83	M	D	S	L	R	P	E	D	T	G	V	Y	F	C	A	R	<u>Q G T</u>			102	
421	<u>ATGGACAGTCTGAGGCCGAGGACACGGGCGTGTATTCTGTGCAAGACAAGGAACTATA</u>																				480
103	A	G	I	R	H	W	G	Q	G	T	P	V	T	V	S	S					122
481	<u>GCAGGGTATACTCGGCCAAGGGACCCCCCGTCACCGTCTCCTCAGGTGAGTCCTTA</u>																				540
541	<u>CAACCTCTCTTCTTACTGCTAAATAGATTTACTGCATTGTGGGGAAATGT</u>																				600
601	<u>GTGTATCTGAATTCTAGGTCTATGAAGGACTAGGGACACCTTGGAGTCAGAAAGGGTCAT</u>																				660
661	<u>TGGGAGCCCCGGCTGATGCCAGACACATCCTCAGCTCCAGACTTCATGGCCAGAGAT</u>																				720
721	<u>TATAGGGATCC</u>																				731

*Bam*HI
TATAGGGATCC

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FIG. 11

Hirudini

1	AAGCTTATGAATAATGCCAATCCTACATGGTAAATATAGGTTGTCTATAACC	59
60	ACAAACAGAAAAACATGAGATCACAGTTCTACAGTTACTCAGCACAGGACCTCA	119
-19	M G W S C I I L F L V A T A T	-5
120	CCATGGGATGGAGCTGTATCATCCCTCTTCTGGTAGCAACAGCTACAGTAAGGGCTCA	179
180	CAGTAGCAGGCTTGAGGTCTGGACATATATGGGTGACAATGACATCCACTTGCCTT	239
-4	G V H S Q V Q L V E S G G V V Q	13
240	CTCTCCACACGGTGTCCACTCCCAGGTCCAACCTGGGACTCTGGAGTCTGGAGGGCTGGCAG	299
14	P G R S L R L S C S S G F I F S <u>N Y G</u>	33
300	CCTGGAAGGGTCCCTGAGACTCTCTGGATTCATCTCAGTAACTATGGC	359
34	<u>M A</u> W V R Q A P G K G L E W V A <u>T I S H</u>	53
360	ATGGCCTGGTCCCCAGGCTCCAGGCCAAGGCAATGAGGGCTGGAGTGGCAACCATAGTCAT	419

CDR 1

CDR 2

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FIG. 11 (cont'd.)

FIG. 12

-19	HindIII	M	G	W	S	C	I	I	L	F	-11
1	AAGCTTACAGTTACTCAGCACACAGGACCTCACCATGGATGGCTATGGCTATCCTCT	60									
-10	L	V	A	T							-5
61	TCTGGTAGCAACAGCTACAGGTAAAGGGCTCACAGTAGCAGGCTTGAGGTCTGGACATA	120									
-4					G	V	H	S	Q	V	2
121	TATATGGGTGACAATGACATCCACCTTGCCTTCTCCACAGGTGTCCACTCCAGGTC	180									
3	Q	L	V	E	S	G	G	V	V	Q	22
181	CAACTGGGTGGAGTCTGGTGGAGGGCGTGGCAGGCTGGAAAGGTCCCCTGAGACTCTCCTGT	240									
23	S	S	S	G	F	I	F	S	[N Y G M A]	W	22
241	TCCTCCCTGGATTCACTTCAGTAACATGGCATGGCTGGCTGGCTCCAGGCC	300									
43	K	G	L	E	W	V	A	T	I	S	42
301	AGGGGCTGGAGTGGCTCGCAACCATTAGTCATGATGGTAGTGAACACTTTCGAGAC	360									
63	<u>S</u>	<u>V</u>	<u>K</u>	<u>G</u>	R	F	T	I	S	R	82
361	TCCGTGAAGGGCCGATTCACTATCTCCAGAGATAATAGCAAAACACCCATTCTGCAA	420									

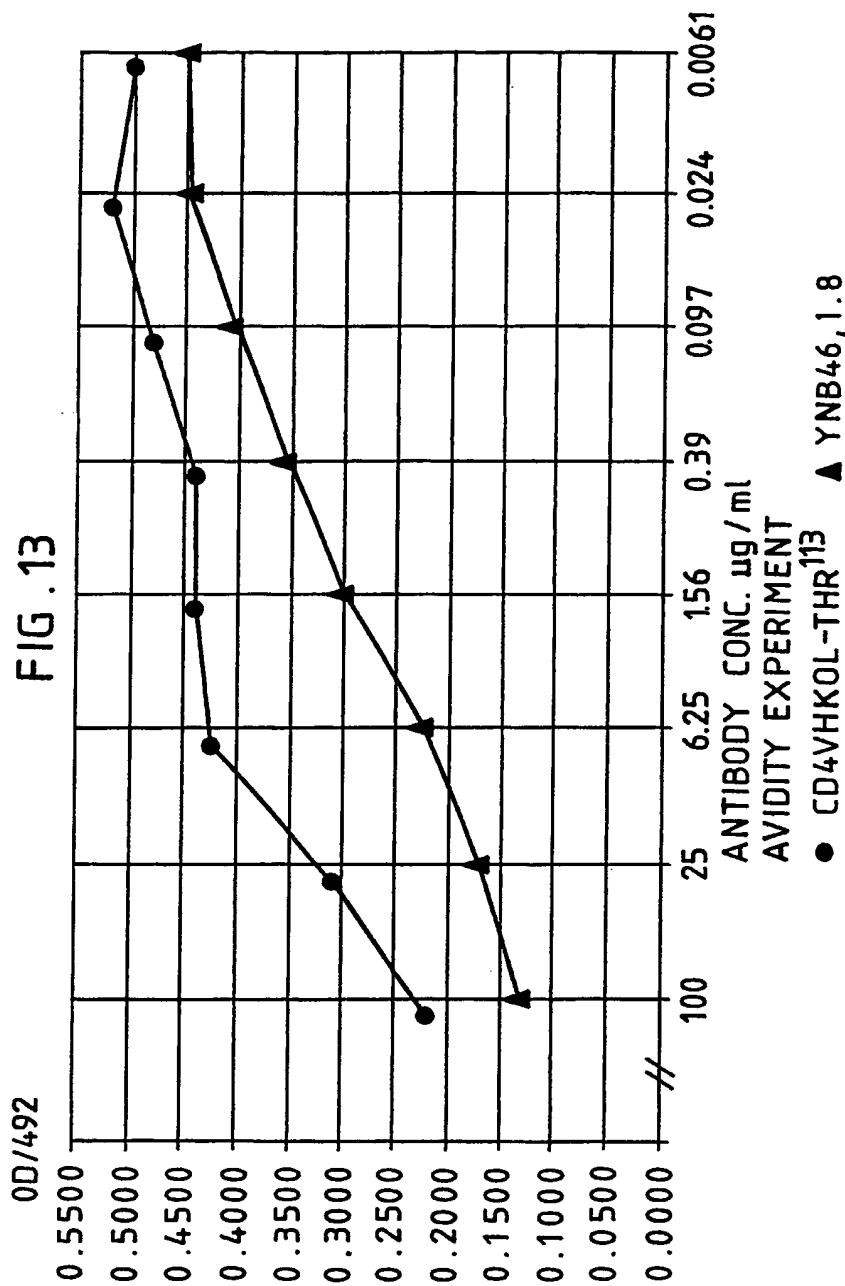
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FIG. 12 (contd.)

		CDR 3	
		Q G T I	
83	M D S L R P E D T G V Y F C A R	102	
421	ATGGACAGTCTGAGCCCCGAGGACACGGGGCTGTATTCTGTGCAAGACAAAGGGACTATA	480	
103	A G I R H W G Q G T T V T V S S	122	
481	GCAGGTATAACGTCACTGGGCCAAGGGACCCACGGTCAACCGTCTCAGGTGAGTCCTA	540	
541	CAACCTCTCTTATTCAAGCTTAAATAGATTACTGCATTGTGGGGAAATGT	600	
601	GTGTATCTGAATTCAAGGTCAATGAAGGACTAGGGACACCTTGGAGTCAGAAAGGGTCAT	660	
661	TGGGAGCCCCGGCTGATGCAGACAGACATCCTCAGCTCCAGACTTCATGCCAGAGATT	720	
			<i>BamHI</i>
721	TATAGGGATCC		731

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FIG. 13



INTERNATIONAL SEARCH REPORT

International Application No PCT/GB 91/01578

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) ⁶ According to International Patent Classification (IPC) or to both National Classification and IPC IPC5: C 12 P 21/08, C 12 N 15/13, A 61 K 39/395						
II. FIELDS SEARCHED Minimum Documentation Searched ⁷ <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="width: 15%;">Classification System</th> <th style="width: 85%;">Classification Symbols</th> </tr> </thead> <tbody> <tr> <td style="text-align: center;">IPC5</td> <td style="text-align: center;">C 12 P; C 12 N; A 61 K</td> </tr> </tbody> </table>			Classification System	Classification Symbols	IPC5	C 12 P; C 12 N; A 61 K
Classification System	Classification Symbols					
IPC5	C 12 P; C 12 N; A 61 K					
Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in Fields Searched ⁸						
III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹						
Category ¹⁰	Citation of Document ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³				
X	WO, A1, 9007861 (PROTEIN DESIGN LABS, INC.) 26 July 1990, see page 5; page 10, line 25 - page 14; page 28 - page 30	1-5				
Y	—	1-9				
X	Proc. Natl. Acad. Sci., vol. 86, December 1989, Cary Queen et al.: "A humanized antibody that binds to the interleukin 2 receptor", see pages 10029-10033, page 10031 right column-page 10033	1-5				
Y	—	1-9				
Y	Nature, vol. 341, October 1989, E. Sally Ward et al.: "Binding activities of a repertoire of single immunoglobulin variable domains secreted from Escherichia coli", see page 544 - page 546	1-9				
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IV. CERTIFICATION						
Date of the Actual Completion of the International Search 16th December 1991	Date of Mailing of this International Search Report 08 JAN 1992					
International Searching Authority EUROPEAN PATENT OFFICE	Signature of Authorized Officer  MISS J. TAZELAAR					

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		Relevant to Claim No
Category	Citation of Document, with indication, where appropriate, of the relevant passages	
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X	EP, A1, 0328404 (MEDICAL RESEARCH COUNCIL) 16 August 1989, see page 4; page 9, line 30; page 11, line 5 --	1-5
X	EP, A2, 0365209 (BECTON DICKINSON AND COMPANY) 25 April 1990, see in particular col. 3, lines 27-49 and columns 5-8 --	1-5
A	Proc.Natl.Acad.Sci., vol. 87, June 1990, J Sharon: "Structural correlates of high antibody affinity: Three engineered amino acid substitutions can increase the affinity of an anti-p-azophenylarsonate antibody 200-fold ", see page 4814 - page 4817 --	1
A	Science, vol. 239, March 1988, M Verhoeven et al.: "Reshaping Human Antibodies: Grafting an Antilysozyme Activity ", see page 1534 - page 1536 --	1-9
A	Nature, vol. 321, May 1986, P T Jones et al.: "Replacing the complementarity-determining regions in a human antibody with those from a mouse ", see page 522 - page 525 page 525, left column --	1
A	Nature, vol. 328, August 1987, S. Roberts et al.: "Generation of an antibody with enhanced affinity and specificity for its antigen by protein engineering ", see page 731 - page 734 --	1

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No
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P,X	WO, A1, 9109967 (CELLTECH LIMITED) 11 July 1991, see the whole document -----	1-9

ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO.PCT/GB 91/01578

SA 51310

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